

Pt. of 24
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 00-450)

PATENT

In re Application of: Polverino et al.)

Serial No.: 09/599,087)

Filed: June 21, 2000)

For: Secreted Epithelial Colon Stromal-1)
Molecules and Uses Thereof)

Before the Examiner: S. Rawlings

Group Art Unit: 1642

DECLARATION PURSUANT TO 37 C.F.R § 1.131

We, Anthony J. Polverino, residing at 2850 Marietta Circle, Thousand Oaks, California, and Roland Luechy, residing at 7300 Worth Way, Camarillo, California, hereby declare:

1. We are named co-inventors on United States Letters Patent Application Serial No. 09/599,087, filed on June 21, 2000.

2. The invention disclosed and claimed in the instant patent application was conceived and reduced to practice in the United States by us before February 1, 2000.

3. We used a proteomic-based approach to characterize a novel protein isolated from conditioned media obtained from squamous cell and colorectal carcinoma cell lines.

4. We first determined the amino acid sequence of the isolated protein and used this sequence to identify EST sequences in both GenBank and proprietary databases capable of encoding the isolated protein. Accompanying this Declaration is a copy of the proteomic analysis performed by us before February 1, 2000 (Exhibit A). In that analysis, the EST sequence disclosed in GenBank Accession No. AA283751 was identified as containing sequences capable of encoding the isolated protein. The date on which the proteomic analysis was performed has been redacted from this document.

5. We then obtained a clone purportedly containing the nucleotide sequence disclosed in GenBank Accession No. AA283751 from the Integrated Molecular Analysis of Genomes and their Expression (I.M.A.G.E.) Consortium, and determined the nucleotide sequence of the clone's cDNA insert. Accompanying this Declaration is a copy of the nucleotide sequence of the cDNA insert as determined by us before February 1, 2000 (Exhibit B). The date has been redacted from this document; however, the date is before February 1, 2000, the date that the FAPESP/LICR Human

Cancer Genome Project (GenBank EST Database Accession No. AW351839) reference was published.

6. The open reading frame of the nucleotide sequence of the cDNA insert (SEQ ID NO: 4) as shown in Exhibit B differs from the nucleotide sequence of GenBank Accession No. AA283751 (Exhibit C). Specifically, the nucleotide sequence of GenBank Accession No. AA283751 contains two mismatches, seven point deletions, and a single point insertion. As a result of these sequence differences, none of the four open reading frames of the nucleotide sequence of GenBank Accession No. AA283751 encodes the full-length human Secs-1 polypeptide (SEQ ID NO: 5) as determined in the proteomic analysis described in paragraph 4 (Exhibit D).

7. We hereby declare further that all statements made herein by each of us to our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: September 25, 2002

Signed: _____


Anthony J. Polverino


Roland Luchny

EXHIBIT B

contig name: zhgb-aa283751-wz.ctg

contig assembler: jojeman

components:

zhgb-aa283751-a

zhgb-aa283751-a2

zhgb-aa283751-b

zhgb-aa283751-c

zhgb-aa283751-d

ahgi-107236-cya (4D)

ahgi-053214-cya (4D)

zhgb-aa283751-ca (99.3%)

assembly done: [REDACTED]

zhgb-aa283751-wz.ctg

VECTOR_MATCH: NONE Fri [REDACTED] 22:59:25 [REDACTED]

VECTOR_MATCH: NONE Fri [REDACTED] 22:59:30 [REDACTED]

OLIGO_MATCH: NONE SEQ Fri [REDACTED] 22:59:31 [REDACTED]

zhgb-aa283751-wz.ctg Length: 829 Fri, [REDACTED] 4:03 PM Check: 5459

POLYA_MATCH: MADE STRAND f

LOC e BEG 802 END 819 Fri [REDACTED] 22:59:33 [REDACTED]

REMOVED f BEG 807 END 829

"AAAAAAAAAAAAACCGCGCCCGC"

zhgb-aa283751-wz.ctg Length: 806 Fri [REDACTED] 22:59:33 [REDACTED] Check: 4601

REPMATCH: status:USEFUL 673 to 806 was Lib:B2 strand f

score 101 basecutoff 100 truecutoff 200 - NOT REPLACED with Ns

zhgb-aa283751-wz.ctg Length: 806 Fri [REDACTED] 23:09:05 [REDACTED] Check: 4601 ..

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1  GGAACGAGGG AAAATCTGCC TTCTCACCAT GAGGCTTCTA GTCCTTTCCA
51  GCCTGCTCTG TATCCTGCTT CTCTGCTTCT CCATCTTCTC CACAGAAGGG
101 AAGAGGCGTC CTGCCAAGGC CTGGTCAGGC AGGAGAACCA GGCTCTGCTG
151 CCACCGAGTC CCTAGCCCCA ACTCAACAAA CCTGAAAGGA CATCATGTGA
201 GGCTCTGTAA ACCATGCAAG CTTGAGCCAG AGCCCCGCCT TTGGGTGGTG
251 CCTGGGGCAC TCCCACAGGT GTAGCACTCC CAAAGCAAGA CTCCAGACAG
301 CGGAGAACCT CATGCCTGGC ACCTGAGGTA CCCAGCAGCC TCCTGTCTCC
351 CCTTTTCAGCC TTCACAGCAG TGAGCTGCAA TGTGGAGGG CTTTCATCTCG
401 GGCTGCAAGG ACCCTGGGAA AGTTCCAGAA CTCCACGTCC TTGTCTCAAT
451 TGTGCCATCA ACTTTTCAGAG CTATCATGAG CCAACCTCAC CCCACAGGGC
501 CTCAGTCGCC ACCATGTGGG CCTCTCCAGT GCAAACCACC GAGCATTCCA
551 CCATGACCGG TCACAGCTAC AAATCCAGAG ACCATCAATC CTGCTAGAGT
601 GCAGGGTGGC AAGCACCCAA GGGTGGCTGA CCAAGACTGC AGAGTCTCCT
651 CCATCTTCAG GTCCATTAG CCTCCTGGCA TTAACTACC AGCATCCAGT
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701 GGTCCCAAG GAATCCCTTC CTAGCCTCCT GACATGAGTC TGCTGGAAAG
751 AGCATCCAAA CAAACAAGTA ATAAATAAAT AAATAAACTC AATGCAGACA
801 CAAAAA

EXHIBIT C

SEQ ID NO:4 vs. AA283751

	40	50	60	70	80
AA283751	ATGAGGCTTCTAGTCCTTTCCAGCCTGCTCTGTATCCTGCTTCTCTGCTT>				
SEQ ID NO:4	ATGAGGCTTCTAGTCCTTTCCAGCCTGCTCTGTATCCTGCTTCTCTGCTT				

	90	100	110	120	130
AA283751	CTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTGCCAAGCCTGGTCAG>				
SEQ ID NO:4	CTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTGCCAAGCCTGGTCAG				

	140	150	160	170	180
AA283751	GCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAACA>				
SEQ ID NO:4	GCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAACA				

	190	200	210	220	230
AA283751	AACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGA-CC>				
SEQ ID NO:4	AACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGA				

	240	250	260	270
AA283751	AGAG-CCCG-CTTTGGCT-GTG-CTGGGG-A-TCCCACAGGTGTAG>			
SEQ ID NO:4	AGAGCCCCGCCTTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAG			

EXHIBIT D

ClustalW (v1.4) multiple sequence alignment

5 Sequences Aligned

Alignment Score = 707

Gaps Inserted = 20

Conserved Identities = 0

Pairwise Alignment Mode: Slow

Pairwise Alignment Parameters:

Open Gap Penalty = 5.0 Extend Gap Penalty = 0.1

Similarity Matrix: blosum

Multiple Alignment Parameters:

Open Gap Penalty = 5.0 Extend Gap Penalty = 0.0

Delay Divergent = 40% Gap Distance = 8

Similarity Matrix: blosum

Processing time: 0.6 seconds

```
SEQ ID NO:5      1      MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRT 37
AA283751-1      1  FGTREN-----LPSHHEASSPFQPALYP-ASLLLHLLHRREEASC----- 39
AA283751-2      1      SERGKICLLTMRLVLSSLLCILLLCFSIFSTEGKRRPANSI----- 42
AA283751-3      1      E-----SRPFIQRR---VML---S---RT---RELRSQ----- 21
AA283751-4      1  GWSL-----LGSLVDHS---ARY---VMCAQ-GSGAKATSP----- 29
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SEQ ID NO:5      38  RLCCHRVSPNSTNLKGHHVRLCKPCKLEPEPRLWVPGALPOV 81
AA283751-1      40  -----QQPGQAGEPGSAATESLAP-TQQT 62
AA283751-2      43  -----VRQENQALLPPSP 55
AA283751-3      22  -----IR-SRQKEM 29
AA283751-4      30  -----IG-CTYCELALS---WVASF---RM 47
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